

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura, Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada, Shigemasa; Takei, Masami

(ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto

(B) STREET: 30 Rockefeller Plaza

(C) CITY: New York

(D) STATE: New York

(E) ZIP: 10112-3801

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

(B) COMPUTER: Compaq PC

(C) OPERATING SYSTEM: Windows 95

(D) SOFTWARE: WordPerfect 8.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/090,672

(B) FILING DATE: 04-JUNE-1998

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/JP97/04468

(B) FILING DATE: 05-DEC-1997

(A) APPLICATION NUMBER: JP-8-325763

(B) FILING DATE: 05-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perry, Lawrence S.

(B) REGISTRATION NUMBER: 31865

(C) REFERENCE/DOCKET NUMBER: 766.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 218-2100

(B) TELEFAX: (212) 218-2200

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCTACCGTT TTTTCCTGC TTTCTATTCC AGGTCAGTCT TCACTGTTTC CG ATG GAA	58
Met Glu	
1	
GAT GGA TTC TTG GAT GAT GGC CGT GGG GAT CAG CCT CTT CAT AGT GGC	106
Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly	
5 10 15	
CTG GGT TCA CCT CAC TGC TTC AGT CAC CAG AAT GGG GAG AGA GTG GAA	154
Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu	

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20	CGA TAT TCT CGA AAG GTG TTT GTA GGC GGA TTG CCT CCA GAC ATT GAT	202
35	Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp	
40	GAA GAT GAG ATC ACA GCT AGT TTT CGT CGC TTT GGC CCT CTG ATT GTG	250
55	Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val	
70	GAT TGG CCT CAT AAA GCT GAG AGC AAA TCC TAT TTT CCT CCT AAA GGC	298
85	Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly	
100	TAT GCA TTC CTG CTG TTT CAA GAT GAA AGC TCT GTG CAG GCT CTC ATT	346
115	Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile	
130	GAT GCA TGC ATT GAA GAA GAT GGA AAA CTC TAC CTT TGT GTA TCA AGT	394
145	Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser	
160	CCC ACT ATC AAG GAT AAG CCA GTC CAG ATT CGG CCT TGG AAT CTC AGT	442
175	Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser	
190	GAC AGT GAC TTT GTG ATG GAT GGT TCA CAG CCA CTT GAC CCA CGA AAA	490
205	Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys	
220	ACT ATA TTT GTT GGT GGT GTT CCT CGA CCA TTA CGA GCT GTG GAG CTT	538
235	Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu	
250	GCG ATG GTA ATG GAT CGG CTA TAC GGA GGT GTG TGC TAC GCT GGG ATT	586
265	Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile	
280	GAT ACC GAC CCT GAG CTA AAA TAC CCA AAA GGA GCT GGG AGA GTT GCG	634
295	Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala	
310	TTC TCT AAT CAA CAG AGT TAC ATA GCT GCT ATC AGT GCC CGC TTT GTT	682
325	Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val	
340	CAG CTG CAG CAT GGA GAG ATA GAT AAA CGG GTA AGC CTT ATA CTA CAT	730
355	Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His	
370	TTT GGA AAA TTC TAGAAATGGT CCTCTAAATG TGTGATTACC AATATTAGAA	782
385	Phe Gly Lys Phe	
400	CGGGAGCATT TTATGACAAT AAAGTGACAG CTGACAATTT TGCCTATAGA GTTAATTATG	842
415	GTCTATAATA CATGAAATAA TGTCCTATGA ATTTCTTTTA TCTTTCAGTT TTTTGAGTAG	902
430	CCTAATCAGA ACACTACAAT TTA CTCTAGAGT TAATTTAATC TTCTCTAACT TCCATTCAAT	962
445	CTCAATCCAT CCGTCCATTC ATTCACCTAG TTTGTAAGTC ATTCAATAAA TATTTACTGA	1022
460	ATCCTTTGTT CTGTGTTATA TCAAGTATAC AAACAGGAAT GCCCTTGAGG TTTCTGCCCC	1082
475	TTTTTTTTGT TTGTTTTTTA ATCCTGGGAC ATAGGGAAGA CCTCAGCAAG CCCTATTTCT	1142
490	CAATGAATTG TACTCACAGA TTTCTTTTTT TTTTTTTTTT TCTTTTTCCA CAGCCGCCAC	1202
505	CTCTCACCGA TTTATTCCTT AGCTTGGTGT TTCATGTATT CAACAAACGT TTTAGTGCTT	1262
520	AGGGCAAGAA GTTCCTGTCC TCATGAGTTT ATTTCTTAGC AGATAGAAGT GTATCACTTG	1322
535	CCAGTACTAC TCAGAGTGTG GCCTGTGGAC TGACCTCCAG TCTGTAAACT TAGTTTGTAG	1382
550	TGAGATAGGA ATTTAGACCA GAATGTGTAA TCAACCACAT TACTGGGCAC AATGTTTGGT	1442
565	CCAGCTGGCG ATTTTTTTTT CATAGAAAGC CTTTATTGAT GAGGGAAGCA ATATATTGAT	1502
580	TTATATTTTG GGGTCACCTT TTTATTTTCAT GGCACACTGG CACTTTCATG CATGCTGACT	1562
595	TTGATATCCA TCACTCTGAG GCATTGTGCT AAAATAGATT GATTTTATCG TGTGTTCTC	1622
610	AATCAAGAT GTAAAAATCA TCAAGTCAGT AGCAGTTTTT GCTTTTTATG TTTTCATGTC	1682

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TGTGAATCTA	TTAAAGAGAA	AAGTATCTGT	TCTATTCTAA	GCATGGGGGA	GGGACAAGAT	1802
TAGTATGTTA	ACATGCCTAC	TTTGTGTTGT	TGAGATGGAG	TCTCTCTCCG	TCACCCAGGC	1862
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GAGCAGCCTA	GAGGCCAGAA	GCCCAGTGCT	CTCCTTATGC	CTGCTCTTCC	TGGGCTTCGT	2342
GACACTCTTC	TTCTCCTTTT	GTA CTTTTAT	TTTTTTAGTT	AAAAAATTTT	TTTTAGAGGG	2402
AGGGTCTCAC	TCTGTCACCC	AGGCTGGAGC	ACAGAATCAC	AATCATGACT	CAC TGCATGT	2462
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TCACATGACA	GGTTGGCCGA	TAGAACGCTG	GAACAGGCC	AGTTTTAGAA	ATTCACCTCT	2702
GACTTTTAGA	CTCAGGTGAA	CCATTCTTAC	TGAGAAAGAA	CAAAGCAGGG	TTTTAGACTG	2762
TGAATCCTAT	GGCTGCATCT	TTTTTTTTTT	TTTAACAGAG	TTCCAGGTTT	GTGATTATAA	2822
CCCAACATGT	GTACACTATA	AATAGAAACC	ACGAGCCAGG	CTTTTACGA	CAGCTCAGAA	2882
TCTTGTGACG	CAGTAGTCAG	GCATCTTCAC	ACCGACTTGA	ATATTGAAGT	GCAGTTGTGT	2942
GGAAC TTGGA	TCATCTTAGT	TGATTTTGTT	TAAATTATGA	TTCCACATAT	GACAAAAATC	3002
CAGATCCACT	AATTAAAATG	AGGGTTTATG	TCTATGAATA	ATCTCCTGTG	GGTTTAATCT	3062
CATAACATT C	TAGTCTAAAC	AGTTGGCTTC	ACTTCATGAT	GTCTGCTCAA	ATCCTTTTTT	3122
CTTTAAAGGA	GTGTTATTTA	ATAAGAAAAA	AAATGTAAAA	TGATAGATAA	TAAAAGCCTT	3182
ACTAGGTTCT	TAAAAGATGA	ACTATCCATA	TTTCAGTAAA	TGAATAATTA	GTCCCTCCTC	3242
TTTGGGCACC	TTGGAACAGA	TTCATTCAGA	TAGTGGGTGG	AAATGTACAT	GTATGGTAAG	3302
CATTGCTGGC	CTAGTCACTG	AAAAATGTAA	ACTCTTATTT	TTGATTGCAG	GTGGAAGTTA	3362
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GGGCTGCTAT	CCATTCTCGT	GCTGGCAGGG	AATTCCACAA	GCCCCTGGTG	AAGGAAGGCG	3542
GTGACCGCCC	TCGGCATATT	TCATTCCGCT	GGAACTAAAG	GATAACTGCA	GTGCTCATTT	3602
TCAGGCCTCA	GAATAAGTGC	ACTCTTCTGT	TCATTCTGAC	CCCTTCCTCA	ACCTCTTCAC	3662
GCTGGCATGT	CCTTTTGTAG	CAGTCTGTAA	CTTAAC TATA	GTATAATGAA	AAGAATGACC	3722
TATAATATAG	GTGTTTTGTA	GATTCTTG TG	TCACTGCAAA	CAATATGAAC	TCCTTTTTTCG	3782
TATTGCCATC	GGGTTGCATG	GAAGTTTTAT	TCTCTTGTTT	TGCTGGAAAC	CAAGAGGATC	3842
CAAAC TTCT	GCAACATTTT	CTTAGAGGAG	AGAGAGAAAT	ATTAAAAGAG	AAATGAAACA	3902
ATAGAGTATT	TTGGGTTTTT	AATTAAATTA	TTGTTAATAA	TATAACATAT	AAGAATACTT	3962
TTATTAAAT	AACCATGCAA	CAATAACACT	ATCGGTCTAT	CTGACAGTTT	TTCCCCCAGG	4022
GAAGTGCTTT	TGCCTTTTCC	TTTCTTTTTT	TTTTTTTTTC	ATCTTTTTTG	TTCTCTCTCT	4082
TTTTTCCATC	CCTTTTTAAT	TTTTTTAACA	GCAATGGAGG	AAGTTAACAA	TTTTTAATGG	4142
AAAGAGCATG	TTAGAGCAAA	CAAATGCATA	AGCAAGACTG	AGCAGCATTA	TAATTAATTT	4202
TCAGGGTTTT	GAGGCTGAAC	ATAATTT CAT	TATCCCTCAA	AAAGTTACCA	CCACATCAGA	4262
AAAAAAAAAA	AAAA					4276

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GTTGGAGGTT CTGGGGCGCA GAACCGCTAC TGCTGCTTCG GTCTCTCCTT GGGAAAAAAT      60
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                                     Met Gly Ser
                                     1
GAC AAA AGA GTG AGT AGA ACA GAG CGT AGT GGA AGA TAC GGT TCC ATC      163
Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile
      5              10              15
ATA GAC AGG GAT GAC CGT GAT GAG CGT GAA TCC CGA AGC AGG CGG AGG      211
Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg
      20              25              30              35
GAC TCA GAT TAC AAA AGA TCT AGT GAT GAT CGG AGG GGT GAT AGA TAT      259
Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr
      40              45              50
GAT GAC TAC CGA GAC TAT GAC AGT CCA GAG AGA GAG CGT GAA AGA AGG      307
Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg
      55              60              65
AAC AGT GAC CGA TCC GAA GAT GGC TAC CAT TCA GAT GGT GAC TAT GGT      355
Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly
      70              75              80
GAG CAC GAC TAT AGG CAT GAC ATC AGT GAC GAG AGG GAG AGC AAG ACC      403
Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr
      85              90              95
ATC ATG CTG CGC GGC CTT CCC ATC ACC ATC ACA GAG AGC GAT ATT CGA      451
Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg
      100              105              110              115
GAA ATG ATG GAG TCC TTC GAA GGC CCT CAG CCT GCG GAT GTG AGG CTG      499
Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu
      120              125              130
ATG AAG AGG AAA ACA GGT GAG AGC TTG CTT AGT TCC TGATATTATT      545
Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser
      135              140
GTTCTCTTCC CCATTCCCAC CTCAGTCCCT AAAGAACATC CTGATTCCCC CAGTCTTCAA      605
GCACATGAAT TCAGAATGAA AGGTTTGCCA TGGCTAAGGA ATGTGACTCT TTGAAAACCA      665
TGTTAGCATC TGAGGAACCT TTTTAAACTT TGTTTTAGGG ACTTTTTTTT CCTTAGGTAA      725
GTAATGATTT ATAAACTCCT TTTTTTTTTT TTGACTATAG TCGGTTGCAT GGTACTTTTA      785
AGCGTGGAAT CAAATGGAGT GGCATTTAGT TCAGGCGGCT TGTTCCCTGC CATGGCAAAG      845
TATCAAGAAG ATCCCCAAGT CAAGTCACAT TTGTAAAGCT GCTTCCCAAT TGGCTTTGTC      905
ACGCAGTGTT GAAGCAGTGG GAGAGAGATT CACCTGTTAT AAAGGAACTG ACTAACACAA      965
GTATCCCGTC TATATCTGAA TGCTGTCTCT AGGTGTAAGC CGTGGTTTCG CCTTCGTGGA      1025
GTTTTATCAC TTGCAAGATG CTACCAGCTG GATGGAAGCC AATCAGGTTG CTTCACTCAC      1085
CAAGTCTAGA TATTCATGAA AATGGAACAA GTCTGTACAA TTTTAAAAAA AGGTTGAAGG      1145
AGTGGTTTGT TCCAAAGGAG TGACTTTTTT TTAATAAAAAA AAGCTTTGTA TATATTAAAA      1205
TTGATGTTAC TAGAATAAGT ACAGTACCAA GGACTTCATT ATAGAATTTG TTCTGCCTTT      1265
AAACATGGCT ACCTACCTGG CAGGGCTTTG TTAACACTG AATACCTGTC TGGTAATCAC      1325
TAAACATCT TAATGTTTCC CTTTTTTCTA GTTTGTTATA TTCCTATTAT GTCCATTGAG      1385
AGTAAGCTTA GTATATCAA CTCTCCATTT GACAGTGAAG AGAACATAGT GAAAGTCTGT      1445
GGCGGCATTT TTATAAGTAA TTCCTTATTT CTGCCTGAAG ACCACAAAGC CTCCTGGAGG      1505
CGTAAGTGCT CAGACCGGTC TTCAGGGAAT ATTTAAGGAC TTAGTGGAAT TTATGAACAA      1565
TAAGTCTGAT GAGATTAGCC TGGGAGTGGT GTCCTGCAGC TGTCTAATCT AGTTAGAGTG      1625
GCATTAACAT TCTAATCTCC TTGAGAATGC CTTTTATAGT CTGTTCAAAG CAAGTCATTG      1685
ATGGTTCTTC GAGGTAGTGT TAACTGAAGT GTTCTTCAGT TTGTCAAGAT AATGTTCAAGT      1745
GCTTGGCACT TAAATAACAT TTTTTCGAAG AACTCCAAGG CACATTATTG AATGCCTTTA      1805
ACCAAGTGCA TTCTGGGAAG TTTGCTTGAC TCATTATCTT GCTTTTCTGC AGCATTCTGT      1865
GATTTGAGTC ATCCATGAAT CCATGAATAA AAGTTACATT CTTTGATTGG TAATATTGCC      1925

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ATTTATAACA	AGACTCACTA	ATGAGGGTAT	CACTTTGACT	GACTGATTTG	TTAAAGTTTT	1985
TAAGCCTCTC	ATTTTCCTAA	CCCAGAAATC	ACAGCCTGAT	TTTATTAAAA	GTAGAGCTTC	2045
ATTCATTTC	TACCATAGAT	ACCATCCTAG	TAAATCCAGA	ACATATACAA	GGTTCATGTG	2105
AGTCTGCTTT	CTTGACATGA	TAGCATTGTT	TGATGCAGTG	GATATGTCAG	AATGACTAAC	2165
CTAGGAGTTT	AAAACCTCCTA	AGAAACTAAA	ACCTGTAAGA	CATTTAAAAG	TCTCCACAAT	2225
TTTAATGTAT	ACAAAGCTAT	GTTACTGTGT	AACACATTAC	AGTTCAAATT	CACTCCAGAA	2285
ATAAAAGGCC	AGTAGGATTA	GGGACTCACT	GGTAGTTTGG	AGTCTCCCAG	CACACATCCC	2345
TCCTAGTGGG	ATGATCTATT	CACATATCTC	CCAGCTTTTT	TATTTTGGCT	TCTGTATATC	2405
ACAGTGAGTG	GATGGCCCTT	CAGCTTTTTT	TCTCCTGGCC	AGACATGCAG	TCTGCCTTT	2465
AGATATCGCA	GAGACAAAAT	TCACAGCATG	TCTTAAATCT	TCCAGGATTT	GCAAGAACCA	2525
AATTGCTCAA	CAGTATGTAT	GTTTAGAGGG	GTTAGACTCC	TTTTTAAAAT	CTGGATATCT	2585
AACCACCTAC	TTAAATCTGT	TTGATAGTGT	CAAACCACCC	CCACCCTTGA	TCCTCCCACC	2645
CCCAAAAAA	AAAAAAAAA	AAAAAAAAA	AAAAAAAAA	AAAA		2689

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTCTCTCTC	TCTTTCACAG	AGTCTTGCTC	TGTCGCCCCAG	GCTGGAGTGC	AGTGGCACAA	60
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GCTGGGACAA	CAGGCACCTG	CCACCACGCC	CGGCTAATTT	TTTGTATTTT	TAGTAGAGAC	180
AGGGTTTCAC	CATGTTAGCC	AGGATGGTCT	CAATCTCCTG	ACCTCGTGAT	CCACCCGCCT	240
CAGCCTCCCA	AAGTGCTGAG	ATTACAGGTG	TGAGCCACCA	CGCCAGCCA	CATCTTTCTT	300
TCTTTCTTTT	TGGTTTTTGT	TTGTGTGTTG	AGACAGGGTC	TTGCTCTGTC	GCCCTGGCTC	360
ACGTGAACCT	CCACCTCAG	CCTCCCAAGT	AGCTGAGACC	ACAGGTGTGA	GCCACCACTC	420
CTGGGTAATG	TTTGTATTTT	TTTGTAGAGA	TGGGGTTTCA	CCGTGCTGCC	CAGACTGCTC	480
TCAAACCTCCT	GGGCTCAAGT	GATCCACCTG	CCTTGACCTC	CTAAAGTGCT	GGAATTACAG	540
GTGTGAGCCA	CCGTGCTCAG	CCGAGTGCT	TTCGTATGTT	TTCTGAGCAC	GTGGATTTCC	600
ATCTCTCTGC	ATTCTCTGTT	CATCTCAGCC	TGTTTGTTCC	ATTGAGATAA	ATGACTTTTT	660
CTTGGAACCT	TAGAGTACTT	TGTGTATTTA	CAGGTTAATC	CCTTATCAAT	TTATATCAGT	720
TGCTGCTATC	TTTTCTTAGA	TTTTTCTTTT	CATTTTAAAA	ATTACATTGT	TTCAATGAAC	780
AGAATTTTTA	AGTTTTAACG	TAGTCCACTT	TGTCCATTTT	CTTTATGACC	GGTGCATTTT	840
AGGGTCTTGT	TTAAGAAATC	GTTCTTTATC	CTGAGGTCAT	AAAGATAGTC	TACTGTATTT	900
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AGACTTACCC	TTCAAAAGGC	CCCATTCACA	AGGCTAGCAC	TTGGCGTGCA	TCTGAGAACC	1140
TGGATTTTGG	GGTGGTTTCT	ATAATGTGGT	GTATGCTGAA	CACCCACCTT	TCCTTCTGGG	1200
AGTCTGGAAT	TTGGGTATAT	GTTGGACAGA	GGCTGCCTAA	GTGACCAGCT	TCAACAACAG	1260
CCCTGGGTGC	TGGGTCACTC	ATGACCCATA	GACAAA ATG	CCA CAC ATG TTG TCA		1314
			Met	Pro His Met Leu Ser		
			1	5		
CAG CTT ATT GCT GGA GGA GTT AGC ACA TCC TGT	GTG ACT GCA CTG GGA					1362
Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys	Val Thr Ala Leu Gly					
10	15	20				
GAG GAA ACT GGT GCC TGG TTC CCT GTG TAT TTG	TCC CAC GCC TCC AGT					1410
Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu	Ser His Ala Ser Ser					
25	30	35				

CCC TTT GCT GAT CTC GTT TTT TGT CCT TTT GCT GAG ATA AAT CAC AGC	1458
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CAG GAG TAT GAC AAT ATG CGG GGT CCT GTG AGT CCT CCT AAC AAA CAG	1506
Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln	
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TTC AAT CTG GGG GTG ATC TTT GGG ATC CCC AAC AAC TGT CGT TTC CCC	1554
Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro	
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Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn	
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TAC CCT TGAACATTCA TGTCTTCATC TGAACATCCA TCTACTACCC CTGATTTTTT	1658
Tyr Pro	
104	
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CGGGCTCCTC ATACCTGCCT GTGTGATTTT TAACATGTCA CGCTATGCAA CCAGTTGCTT	2018
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CTGACCTCAA GTGATCCACC TGCCTCGGCC TCCCAAAGAA CTGGGATTAT GGGCGTGAAC	2498
CACCACGCCA GGTCAGTTT GCAGTGTTT AAATACTGTT GTCTTTGAGA GGAGAGAGGC	2558
ACGCACATAG ACTATGGTGA TTACCATCAT ATACTGGAAA GTGCAAAGTG TAGCGCAGTT	2618
AACTGTGAGC CATCTCATCA AACCCTAACA GATGTCTCAT TTGTCCATAA AGGGGCTTCT	2678
GTCCCATAGA AATTCATGTA CCAACCTAC TCTTCAACCA TGATTTTTCT CTGATGGCCT	2738
GTGTGAACAG ATTAATGGTG TCCATCTAAT TCCTTCCCCA CTGGGGGAAA GCAAATCATC	2798
AGGCCCATTG CAAAACTGC TCTTGGTTGA GCTTCCTGCC TTAAATCATA CCCACAGTGA	2858
ATGGCGTCCC TTTATCACCG CTAATGACTC TGACATCTCT CTCCACTCAC ATGTGAGCCT	2918
CCTCAGCTCT CGATAAACAA GTCTGTCTCG GTTCATTTAT TCTACAAAAA AAAAAAAAAA	2978
AAA	2981

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTCGGCAC GAGCAGCTTT CTAGTTGGAT TAGGCAACAG AATCCTTTGA AAATGTGTGT	60
GCACAGACCA GGTGGCTCTC TGGGCCAGTG TACTCTGAAA GATGTGTGTC CTGGCCTAGC	120
TGGTTGAGGA AAAGCAGGGC AAGCCTAGCC AAATCACACA TCTTGAACAG CCCTCATTCG	180
TTATACTAAC TTTCCACCT TCTGGTGTGT ATAGGAGATA AAGATGGCAG ACGTGCTATT	240
AGGCTGCCAA TGGGAGTGGG CTCTGATATG GTCTTTCAAA T ATG AAT CAC CCC TGG	296

	Met	Asn	His	Pro	Trp	
	1				5	
CAT GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA						344
His Val Cys Phe Leu Ph Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro						
	10			15	20	
ATA TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT						392
Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val						
	25			30	35	
TTA AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA						440
Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile						
	40			45	50	
TCA GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC						488
Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser						
	55			60	65	
ACA ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA						536
Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg						
	70			75	80	85
TTG GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT						584
Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala						
	90			95	100	
GTT GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT						632
Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe						
	105			110	115	
TTT CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT						680
Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						
	120			125	130	
TAAAAAAGT CAGCGTGGCA CGTTTATAGTA TGTGTGGCAG ATCTAAASAG ACAATATTTT						740
GATCTCAGGA GTGTTTATTC TTGAACCACT TTCAGAACTC TAAGATTTGA GAAATAATAA						800
AATATTGACC ATCCTTCAAA GAGAAAAACA CAGGGCGATC TTTGGCATAG CCTGTCATTT						860
TGCTCACATT TCACTTCTCT CTCTCCAAC TCAAGAGCCCC TGCTGTGGAA CAGGTGCTGT						920
GCTGGGTGGC AGGGGAGGTC TCTGGCTTTT TTTTTTTTGG ATCTCCGTCT TAACATCTAG						980
CCTACTGGAG GAAGTGATT TAATCATCCA CTTATCTGTT AACAATTATC TCTGAGGGCC						1040
CGTCACATTC AGAGAAGATT CTAGGTCTC TACAAGTATC CTCTCACTGT GTACATACTA						1100
AATCAACATC CTGCTGGATT TCCCCAGAC ATCTCCCTTC ATCACCATTG GAGAGTATCC						1160
TCTAATTGCC AGCCCTATTC ACCATACTCA TCTCATTTGA TCTGGAGTTT TCTGAGAGTG						1220
ACCGGGGGTG GGATGGACAG GATAATTTAG CAAGAGTGTA TAAGTAAAT CTATATAATA						1280
AAAGTTATCT CCCTGTGCCC CCCATGATCT ATTCTTTATG TAGCAGTCTG AATGAGATTT						1340
TCAGAAACAA GAACCACTTT ACCTTAGTCT CTTCTTCTTC TTCTTCTTCT TTTCTTTTCT						1400
TTTTTTTATG TATTATGGC AACAGAGCAA GACCCAGTCT CAGGAAAAAA AAAAAAAA						1460
A						1461

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGCGCCCGG CCAGAATACC CTATCCTTAA	60
ACATGAATTT AGGGGAGGGG AGGACACAAT TCAATCTATA ACAACTATCA CTGGCTGATT	120
TTGGCAGAGG CCTGTGGCCT CCAGTATTTT GAGGGAGCTG AGGGCCACTG ATCTCTCCAT	180

ATGCTCTCAA	CATCATGGGA	CTAGTAGGAT	GAAAGCAAGC	CTCAGACCAG	ATTCTACCTC	240
AAGCAGGCAC	ACAAACATTC	ATGCAGCTTC	TACTTGGAGC	CTGATGAAGT	TCAAATTGTT	300
TGTCCTCTGA	GGCTCTCTTT	GCATGGAAAT	TTCTCCCATG	ACAGATGAGA	AAGTTCTGGG	360
GCAGCATTCA	GCTTTCTAGT	TGGATTAGGC	AACAGAATCC	TTTGAAAATG	TCTGTGCACA	420
GACCAGGTGG	CTCTCTGGGC	CAGTGTACTC	TGAAAGATGT	GTGTCTCTGGC	CTAGCTGGTT	480
GAGGAAAAGC	AGGGCAAGCC	TAGCCAAATC	ACACATCTTG	AACAGCCCTC	ATTCGTTATA	540
CTAACTTTCC	CACCCTCTGG	TGTGTATAGG	AGATAAAGAT	GGCAGACGTG	CTATTAGGCT	600
GCCAATGGGA	GTGGGCTCTG	ATATGGTCTT	TCAAAT ATG	AAT CAC CCC TGG CAT		654
			Met	Asn His Pro Trp His		
			1	5		
GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC	CCA ACT GCA CCA ATA	702				
Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr	Pro Thr Ala Pro Ile					
10 15 20						
TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT TTA	750					
Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu						
25 30 35						
AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA TCA	798					
Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser						
40 45 50						
GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC ACA	846					
Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr						
55 60 65 70						
ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA TTG	894					
Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu						
75 80 85						
GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT TTT	942					
Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe						
90 95 100						
GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT TTT	990					
Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe						
105 110 115						
CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT TAAAAA	1041					
His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						
120 125 130						
AAGTCAGCGT GGCACGTTTT AGTATGTGTG GCAGATCTAA AGAGACAATA TTTTGATCTC	1101					
AGGAGTGTTT ATTCTTGAAC CATTTTCAGA ACTCTAAGAT TTGAGAAATA ATAAAATATT	1161					
GACCATCCTT CAAAGAGAAA AACACAGGGC GATCTTTGGC ATAGCCTGTC ATTTTGCTCA	1221					
CATTTCACTT CTCTCTCTCC AACTTCAGAG CCCCTGCTGT GGAACAGGTG CTGTGCTGGG	1281					
TGGCAGGGGA GGCTCTGGC TTTTTTTTTT TGATCTCCGT CTTAACATCT AGCCTACTGG	1341					
AGGAAGTGTA TTTAATCATC CACTTATCTG TTAACAATTA TCTCTGAGGG CCCGTCACAT	1401					
TCAGAGAAGA TTCTAGGTTT TCTACAAGTA TCCTCTCACT GTGTACATAC TAAATCAACA	1461					
TCCTGCTGGA TTCCCCCAG ACATCTCCCT TCATCACCAT TGGAGAGTAT CCTCTAATTG	1521					
CCAGCCCTAT TCACCATACT CATCTCATTT GATCTGGAGT TTTCTGAGAG TGACCGGGGG	1581					
TGGGATGGAC AGGATAATTT AGCAAGAGTG TATAAGTAAA ATCTATATAA TAAAAGTTAT	1641					
CTCCCTGTGC CCCCCATGAT CTATTCTTTA TGTAGCAGTC TGAATGAGAT TTTCAGAAAC	1701					
AAGAACCACT TTACCTTAGT CTCTTCTTCT TCTTCTTCTT CTTTTCTTTT CTTTTTTTTT	1761					
AGTATTATGG GGATCTGTTT CTGTTGCCCA GGGTGGAGTG CAGTGGTATG ATCTTGGCTC	1821					
ACAGCAGCCT TGAACCTCCG GGCTCAAGTG GTCCTCCTGC CTCTGCTTCC CTAGTAGCTA	1881					
GGACTGCAGG TTTGTGCCAC CACACCTGGC TAATTGAAAA AAGAAATTTT TTTTCAATAG	1941					
AGACAGTGTC TTGCTATGTC CCCAGGCTGG TCTCAAACTC CTGGCCTCAA GTGATCCTCC	2001					
TGTCTCATCC TCCCAAAGTG TTGGAATTAC AGGTGTGAGC TACTATACTC GGCCAGTACC	2061					
CTTCTCAAAA CACTTCAGCA CTTCCCATTG CACTTGGGTT GAAATTCCCA CCACTCACTG	2121					
GGGCCCCACAA GACTCTTCAA GACTGAATCC TTGCTCAACA TTGTGACCTG CCCCTACCA	2181					
CCTGCAGCCT CACTTGCTGT GCTCCAGCCA TGTGGATCTT CCTCCTGTCT CTAAAACTGC	2241					
CTCAGGTCAT TTGCACCTGC TGTTCTTCCC AAAGGCTGTG TGATTTCCAT CAGTCAGTCT	2301					



TAGCTCGTAT	ACCTCCTTGG	AGACACCTCT	TCTGACCAAC	CAGTCCAAAG	AATCTCCTCT	2361
TATCATGTCA	CTCTGTTTTA	TTTATTTATT	TAGAGATGGA	GTCTCGCTCT	GTCACCCAGG	2421
CTGGAGTGCA	GTGGCGCGAT	CTCTGCTCAC	TGCAAGCTCC	ACCTCCTGGG	TTCATGCCGT	2481
TCTCCTGCCT	CAGCCTCCTG	AGTAACTGGG	ACTATGGGCA	CCCACCACTA	CACCCGGGCTA	2541
ATTTTTTGTG	TTTTTAGTGG	GGATGGGGTT	TCACTGTGTT	AGCCAGGATG	GTCTTGATCT	2601
CCTGACCTTG	TGATCTGCCT	GCCTCCACCT	CCCAAAGTGT	TTTATTTATT	TTAAAGGCAT	2661
GTATCACTCT	CTGAAAATTA	GCTTCTTTCT	TCTTTTTCCT	TGTTATCATC	CATTTCCCCG	2721
AACCAGAATA	GAAGTTCCTG	AGGCCAGAAC	TTCTGTCTCT	CTGCCCCTCA	CTATGTGTCT	2781
CTGGCACATA	CCCCAGTGCC	TGCCTGCTCT	AAAGTAAAT	CTTAGTAAAT	ATTACTGTTG	2841
ACTAAATAAA	TGAATAAATC	CCTTTTAATG	CCCCTTTGGA	AGTTGCCAAG	TAAAGAATAG	2901
GATCCCTTTT	TAAGATTACA	CTTTTGGCTA	TTGATCTGTG	TGTCTGGAAC	AAGATACAGT	2961
TTGAAGATAC	TACCATGGGA	CATGACATCA	GTTGAGCTGA	TTAAGGTTTT	AGTAATAAGA	3021
ATCCAGGATG	TGTCCGGGTG	CGGTGCTCAC	GCCTGTAATC	CTAGCATTTT	GGGAGACCGA	3081
GGCGGGCAGA	TCACGAGGTC	AGCAGTTTGA	GACCAGCCTG	ACCAACATGG	TGAAAACCCCG	3141
TCTCTACTAA	AAAATACAGA	AATTAGCCGG	GTGTGGTGGT	GTCCACCTGT	AGTCCTAGCT	3201
ACTCAGGAGG	CTGGGGCAGG	AGAATTTCTT	GAACCCGGGA	GGCGGAGGTT	GCAGTGAGCC	3261
GAGATCACAC	CAGTGCACTC	CAGCCTGGGC	AACAGAGCAA	GACCCAGTCT	CAGGAAAAAA	3321
AAAAAAA						3329

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGA	ACTGGG	AGTC	AGGTGG	TTGA	CTTG	TGTG	CCTGG	CTGCA	GTAG	CAGCGG	CATCT	CCCTT	60
GCAC	AGTTCT	CCTC	CTCGGC	CTGCC	CAAGA	GTCC	ACCAGG	CC	ATG	GAC	GCA	GTG	114
									Met	Asp	Ala	Val	
									1				
GCT	GTG	TAT	CAT	GGC	AAA	ATC	AGC	AGG	GAA	ACC	GGC	GAG	162
Ala	Val	Tyr	His	Gly	Lys	Ile	Ser	Arg	Glu	Thr	Gly	Glu	
5					10				15				20
CTT	GCC	ACT	GGG	CTG	GAT	GGC	AGC	TAT	TTG	CTG	AGG	GAC	210
Leu	Ala	Thr	Gly	Leu	Asp	Gly	Ser	Tyr	Leu	Leu	Arg	Asp	
				25					30				35
GTG	CCA	GGC	GTG	TAC	TGC	CTA	TGT	GTG	CTG	TAT	CAC	GGT	258
Val	Pro	Gly	Val	Tyr	Cys	Leu	Cys	Val	Leu	Tyr	His	Gly	
			40					45				50	
ACA	TAC	CGA	GTG	TCC	CAG	ACA	GAA	ACA	GGT	TCT	TGG	AGT	306
Thr	Tyr	Arg	Val	Ser	Gln	Thr	Glu	Thr	Gly	Ser	Trp	Ser	
			55				60				65		
GCA	CCT	GGG	GTA	CAT	AAA	AGA	TAT	TTC	CGG	AAA	ATA	AAA	354
Ala	Pro	Gly	Val	His	Lys	Arg	Tyr	Phe	Arg	Lys	Ile	Lys	
			70				75				80		
TCA	GCA	TTT	CAG	AAG	CCA	GAT	CAA	GGC	ATT	GTA	ATA	CCT	402
Ser	Ala	Phe	Gln	Lys	Pro	Asp	Gln	Gly	Ile	Val	Ile	Pro	
			85				90				95		100
CCA	GTT	GAG	AAG	AAG	TCC	TCA	GCT	AGA	AGT	ACA	CAA	GGT	450
Pro	Val	Glu	Lys	Lys	Ser	Ser	Ala	Arg	Ser	Thr	Gln	Gly	
				105					110				115

ATA AGA GAA GAT CCT GAT GTC TGC CTG AAA GCC CCA TGAAGAAAAA	496
Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro	
120 125	
TAAAACACCT TGTACTTTAT TTTCTATAAT TTAAATATAT GCTAAGTCTT ATATATTGTA	556
GATAATACAG TTCGGTGAGC TACAAATGCA TTTCTAAAGC CATTGTAGTC CTGTAATGGA	616
AGCATCTAGC ATGTCGTCAA AGCTGAAATG GACTTTTGTA CATAGTGAGG AGCTTTGAAA	676
CGAGGATTGG GAAAAGTAAT TCCGTAGGTT ATTTTCAGTT ATTATATTTA CAAATGGGAA	736
ACAAAAGGAT AATGAATACT TTATAAAGGA TTAATGTCAA TTCTTGCCAA ATATAAATAA	796
AAATAATCCT CAGTTTTTGT GAAAAGCTCC ATTTTTCAGT AAATATTATT TTATAGCTAC	856
TAATTTTAAA ATGCTCTGCT TGATTGTATG GTGGGAAGTT GGCTGGTGTC CCTTGTCTTT	916
GCCAGTTCT CCAC TAGCTA TGGTGTCTA GGCTCTTTG GGATTTTGA AGCTGTATAC	976
TGTGTGCTAA AACAAAGCACT AAACAAAGAG TGAAGGATTT ATGTTTAATT CTGAAAGCAA	1036
CCTTCTTGCC TAGTGTCTG ATATTGGACA GTAAAATCCA CAGACCAACC TGGAGTTGAA	1096
AATCTTATAA TTTAAAATAT GCTCTAAACA TGTTTATCGT ATTTGATGCT ACAGGATTTG	1156
AAATTGTATT ACAAATCCAA TGAAATGAGT TTTTCTTTT ACCTTCTT GCCCCAGTTG	1216
TTTCTACTAC ATGGAAGACC TCATTTTGAA GGGAAATTC AGCAGCTGCA GCTCATGAGT	1276
AACTGATTTG TAACAAGCCT CCTTTTAAAG TAACCCTACA AAACCACTGG AAAGTTTATG	1336
GTTGTATTAT TTTTAAAAA AATTCCAAGT GATTGAAACT TACACGAGAT ACAGAATTTT	1396
ATGCGGCATT TTCTTCTCAC ATTTATATTT TTGTGATTTT GTGATTGATT ATATGTCACT	1456
TTGCTACAGG GCTCACAGAA TTCATTCACT CAACAAACAT AATAGGGCGC TGAGGGCATA	1516
GAAGTAAAAA CACCTGGTCC CTGCTCTCAG TTCCTGTCT TGTTGGACGA GAAAACAATA	1576
ACGATAAAG ACAGTGAAAG AAAATAACGA TAAAGACAG TGAAAGAAAA TAACAATAAA	1636
AGACAAGGAA AAAATAACAA TGAAAGTTGA TAAGTACATG ATAAGCGAGG TTCCCCGTGT	1696
GTAGGTAGAT CTGGTCTTTA GAGGCAGATA GATAGGTCAG TGCAAATACT CTGGTCCATG	1756
GGCCATATGA AAAGGCTAAG CTTCACTGTA AAATAATAAC TGGGAATTCT GGGTTGTGTA	1816
TGGGTGTTGG TGAACCTGGT TTTAATTAGT GAACCTGCTGA GAGACAGAGC TATTCTCCAT	1876
GTACTGGCAA GACCTGATTT CTGAGCATT AATATGGATG CCGTGGGAGT ACAAAGTGG	1936
AGTGTGGCCT GAGTAATGCA TTATGGGTGG TTTACCATTT CTTGAGGTAA AAGCATCACA	1996
TGAACCTGTA AAGGAATTTA AAAATCCTAC TTTCATAATA AGTTGCATAG GTTTAATAAT	2056
TTTTAATTAT ATGGCTTGAG TTTAAATTGT AATAGGCGTA ACTAATTTTA ACTCTATAAT	2116
GTGTTTCATC TGGAATAATC CTAAACATAT GAATTATGTT TGCATGTTCA CTTCCAAGAG	2176
CCTTTTTTTT AAAAAAAGCT TTTTTTGAAT CATCAAGTCT TTCACATTTA AATAAAGTGT	2236
TTGAAAGCTT TATTTAAAAA AAAAAAAAAA AAAAAAAAAA	2276

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAAA ATGTTAGGGC TTAATATTAT TCATAGATCG AGGATAGTTT CATTCTTAGT	60
CGCCTCCTTA GTCACTCTTC CTATACCAAT CTGAGACCAT TTTACAATTT AGAAAAGACA	120
AATAACTGGT TGGGTACTT GATAGTATAA TAACC	155

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
 GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60  
 GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120  
 AGGTCCATCC AGAAATTGGC TTCAAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180  
 CAGAGCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240  
 AGTGACTCAG GAGATTTAGA AGCGTTAGAG GGAAAGGA 278

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
 TTCTGACAAT GAGTAAGAAG AAAGAGGGTC TTGCCCTTTG GTTATTAAGA TTTATCATAG 60  
 AGCAATAATA ASTAAATCGG TGTATACCA GCACAGAGAT TAGACAAATA AACCAAGGGA 120  
 CTGGACTAAA TAAGC 135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
 ATGGTACCCA GTTTCAAATT AACATGGTGA TTTTACTTGT GTTCCCAAAT TTAACATTAG 60  
 GGAATTTTTG GTTGTGGGTC TGTTATCACT AGAAAAATAT ATATATTGGT GCTGAAGATA 120  
 ATTTTGAGAT AATTAGACAA GACAGTTTAG CATTACAAG AACAGTTTG GCAGTTGAAG 180  
 AATCTATTTA TATGACT 197

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
 CCACCGCACC TGGCTGATGC TTTTCTATCT GACTTCTTTC AGAGGACCCT GAAAGACACT 60  
 AAGTGGAATC TTTCCTTGAA GTCTCCAAG CTAAAACAAT TCTCTGGAAA GATCACCTCT 120

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
CGTTTACAGA TTCTCTTGGC GCTGGCGGTG GAACTACAAA GGGATCGGTG CCTATATCAC 60
AATACCAAAC TTGATAATAA TCTAGATTCT GTGTYTCTGC TTATAGACCA TGTTTGTAGT 120
AGGTAAGAGG AAAACTTCCT ATATTCTGAA ACAGCCTAAC ATTTTACAAA ATTTTAGTTT 180
TCTTTTTTAG AGTCTTATCC TGTAGCTATA TAACAGTTCA TGTCTGATT AGCATTTGTT 240
CACGAGTAAA GCTGGAATA TGAAAATTGA AAAT 274
```

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GATTAGGTGA CCTTCCTTGA ARAGCCACGG GTTCCCATA TCGAAATGCT ATTCATTACC 60
CGAGTCACCT ANGTTCTTAC AAAGGAAGCG AGAAAATTGC TTTTGTGGG CCATGCCCTT 120
TTTGCANAGG TTCCTAAGTA TAGTCGCCAN AATTTTTTTA ATGGCCTAAA G 171
```

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
AGGGGCGCTT GTTCTGCTCT CAGCAGATTG GTTACACGCG TCAGGTGGTG GCGATGACTT 60
AATTCCTAGC CCAAGAAGAA TATAATGTTA AACTGGTTA TGTAATTTT GTGCCTCTCC 120
TTTTTAATGC AGTATTTAGT TCAGATGTTG GCGATTTTTC A 161
```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
 TATAAGGWGG GAACCTTACT ATCTCTAATG ACCTTACTGA TGCTGACTTT AATACTCTGT 60  
 GAAGGTTAGA GTTCAGTGAA TGTTACCTAG AACAGCCCC GGCTGTGGAA TACTTTATTC 120  
 TTAGCCCTAT ATTTGGGGTT TGGATGTCCA CTGTGCTGGT TCCCAGAGAT AGTAAGGGGA 180  
 TGAGAGTATT GGTACATCT CCTGACCCAC ATACTTAAGA TCCAGATGAA CAAGACAGTT 240  
 TTCCTCCTG CTTGGTAGAA CCTATTGYK SHAGGAAACA GYTCCTAAAG AATGGTTCTA 300  
 GCCAGACCCT GTCGYTACCA GAA 323

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
 AGTATGACAA ATAGTTTCTG CCTGATTGGT GAGATTGGG ATGGGCCCCC ACTTTGTTTC 60  
 TCTTTCTGCA TAAAAATTC AACATTTTA CAAAATTTT AAAAACTTCT CCTCAGTCTG 120  
 TACATCTTTG TTAATCAG 138

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
 TGATCCCCAC AATTTCTTGT GATTGGTGAG GAACTATAAA TGACTCCCAT CCAAGCTTAT 60  
 ACCAGAAAAA AGGAGCACAT TTTCTACAAA TTATATCATT TTTAATCCAT TACCACATTA 120  
 TTTTAGGGGA ACTAC 135

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
 CTGAGAGGAG CCATGTATAC AAACCACTTT TTCTAACATG GTCTTTATTA AACTTTGAAT 60  
 ATAAGTACAC CTGCTCGAAG TGTTTCATCTA TATTATTTAA GAACAAGCAA CTGTAAAAA 120

GTAAATCAC AAAAGGTAAG TTGTGGAAG ACAACAAAA AGAATTACTA TATCTGATCC 180  
TGCGTGTTTA TTTTAGAATC TGTTAATAGG CCTACAGCT 219

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACAGTGAGTG TGGCTGAAAC CTAAGCTGAA GGAAGGGAGG AGCAGGCACT GCCATGAGGG 60  
GTCCCTGGAC AGAACTCTT CAGCAGGCCT TGAAGTTAG TTCAGGGGCT ACATGGAATA 120  
CCACTATTTA GCACACAGGT GTGATCTGAG GTGAGGGACT ACCTTTTCGA TCTTGGTTTT 180  
CTCATTTATT T 191

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGAGGTGA AGGGAAGGAA AGAAAGGAAA AACTATCTAC CTGGCAGGAA AAGAGATAAG 60  
CTCCAAGAA CACCAAGCA GATGATGAGT CTAGCTCTAC CCAGCCTCC TCCCCACGAA 120  
TCCAGATCAT AGTAAGAAAC TCTGGGCT 148

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACCACCAG AAATGAACAA AAAGCATTTT ACCTAAAAAT ACACCAGCAA AATGTACTCA 60  
GCTTCAATCA CAAATACGAC TGCTTAAAC CGCAGAAATT TCCTCAACAC TCAGCCTTTA 120  
TCACTCAGCT GGATTTTTTC CTTCAACAAT CACTACTCCA AGCATTGGGG AACACAACCT 180  
TTAATCATAC TCCAGTCGTT TCACAATGCA TTCTAATAGC AGCGGGATCA GAACAGTACT 240  
GCATTTACTT GCCAACAGAA CAGACAGACC TGAAGTCAAG ACAACTGCAT TCTCTGTGAA 300  
GTCTGT 306

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
GTAGCATTTT GGCAGAACCA TTGTTAATTA AAGGGACTTY TGGACCGCAA CYTTAATGTA 60
CCAGATTATT GAGCRGCCCA ATGAATGCTT CATTCTCATT GTTTAAGGTG CTGCTTTGAT 120
TTTTTTTTC AATTCTTTGTA CTATTTTSTA TTTTTTGGAG AGGCACATCC CCAAATTTGG 180
ATGAGGTATT TGTGATAAA TAATTCATCA ATTTCCACAA TGCAGACAAA AATGTCTGCC 240
CAGAGTGGAA AAATAAAACA AGGGGGAGAA GAGTTTGAGT AACGGAGAAG TTCTGTGGAA 300
TCCTAGTGAC AAAAGTTGAG AAACCTACCTT TAAATAAGAC AGTGAGGTAA CAAATGT 357
```

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 219 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
TGGAATAGCC AGGAGAATTC TGGAAAAGTA GAATAATGAG GTAGGGCTTC CCTTCGCTAT 60
TTTGAAGTGC AGATTACACT ATGTAAAACC ATTAGGAACT GGCACGTGAA TAGACAGATC 120
AATAGTTAAT AGCTGTATTA GCCAGAAAAT GGTGTAAGGA CAACAGGCTA ACTAACCCCTG 180
TCACTTGTTA TGCTAAAATT AAGTCTAGAT AGAGTCCTC 219
```

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 251 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
TGAAAGGGGA ATAGAAGCAC AAGAGTCAGT AATCAATAAC AAACAACCTCA AGGTGCTCCT 60
TCCTTACACT GGTGTTCCCC AAAGTGAGGT GAATTGCCAG CCACTGGGAG TCAGGGCCAG 120
TTACATAAGA CATTCTCGGT AAGCCCCCTT TGGGTATCCC AAATAAGGAC TGGGGTGGGT 180
TTATGTGTAG TCCATTATTA ACAACTAAAC GAACAAACCT AGTGAATTGC AATAAATTCA 240
CACCAACAGA A 251
```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 233 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

GTTGAAAGAG TCCTTGGAAG GCTTTTAGAC CAAACCCCTC TGCATGCTCA ARCCTTGGGT 60
ACAGGATTTC TAAGAAGTGG AACAGTCTCC AGGGGTGTGG ARCTCATCGC TCAAGGCAGG 120
TTATCTTATC TGAATAATTT TGTCTGTTGA CTATTGGGAT AGTTCTCCTT CAGATGAGCT 180
GAAATTTTCT CCATAGCTTC CTCTATTAAA CCCAATTCCA CTTCTCAGGG TCA 233

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

CAAAAGCGCT GAAGTTAAGC ATTAATACGC CAGATTCATG ATTTATGATC AGTATCCAAA 60
ACTCCAATA CAAACAATGC AAAGTAGTGC TCCTCAGTAT TATTTTTCGA ATTGTTAGTA 120
ATGTTAAGCA TCAAGGAAAA TAAACACAT CATTGCACAT TACAGCCGCA AAAAAC 176

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

AGAGAGTAAA GCAAGCTATT TTGACAGCAA CCTAATAACA GCTGTCTTCT TCCACTTCTT 60
GGCTAACTCA TCCCCCAGAT AGCCTTCTTT TCTCTTATCA ATTCCCTGTT GCAACAATAA 120
TAAATGCCAC ACCTGATGGA GTCATTAGGC ACTTTCCTAG TGACAAGTGC CTAGGACAGA 180
GGAGAAAACA AAGAAACACT GACAACCACT GAAACTGAC ATATCAGGCC AGGCATGTCA 240
C 241

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

GCTGGAGAGG TGGTGATGTT GCTGAATAAT TGCTTTTAA AGCTGGAGGG GACTTCCAAG 60
AGTCTCTCAT TTAAGAARAA AAATTAAAGA CATAATTGGT AACGGTTTGT ACTGCTGCAG 120
AGGCAACACT TTGCTCACAA TCCTACAGAT CTACTTCACC TGTAACATA ATTTTCCTGA 180

```



## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

AATCTTAGCA TAATGCTTCC TGGGAAATTC TGAAATTGAT TCCATTTCTG CCGTTACAAA 60
CACACACGAA GTTCTAGTT CACTGGGACT TCCTGATTG TTCTTTTAGC TTGCTCCTTC 120
TCACCTAGAA GCTCTGTTTA TTTCTGAGCA ACCCTGGGGC TTGTCTCATA GGACAGGATT 180
TATTATCTC ATCAAGGCTG AGTGTGCCTT AGGAAGTCAT AAACATAAAA AGA 233

```

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

TATAGACAGG GTAGGGACGA TTAGCCCCTC GACAACTTTT CACAAATATA CACACGTTTA 60
ACTACCTCTC AGGTCATGAT AAAGACCGGC CGGGCAGAAA CACTGTAATC CCAGCTACTC 120
GGGAGCCTGA GGCATGAGAA TCACTTGAAC CTGGGAGGTG GAGGTTGCCA TGAGCCGAGA 180
TCACGCCATT GCACTACAGC CTTGGCGACA AGAGTGAAAC TCCATCTG 228

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

GCTTATGATT ACAAACATCC CTCATATGAA AATCTCAGCA TTTNCTGGCT GCTGCCTTCA 60
ATCGCTTTTT CTGAAATAGG TATCCCTTGA TGTCGACTAT TTGATTTTCA CCAGTCGTTT 120
CTCTCTGGCA GTGCTCCCTG CAAATGTGTC CTTTCAAGAA AACAAAACCT GCAAGTGGCT 180
TGTAATGTAC CATGACCTTA TCATGTGAAG GACAAATGGC TCTTGTGCTT ATTAGATAGC 240
AGATGAACTG ATGAACTGAA TTCTTGCTCT GAAGCTTTGA TAAGGTCAGA TGTCTTTG 298

```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (i) MOLECULE TYPE: cDNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human  
 (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

ACTTCGAAGG GAAAAAGAGG AAGGAAAAGG ACTGTTAATA AAATAACAAA GGCAGCAATC 60
AGAATGAACC AGAGCCAGGA CAGCGTAAAG GCTAGGTTCA CAGTGAGATG AAAGAACCTG 120
AAAACAAGTT TAAAACTCAA AAGAGGATTA TTCTCAAGTT ATACTACAGT GAAAAACAT 180
GGAAAAACAC AAAAAGGACA GGCAATAAGG CACAGGCATA CATACAAGGC AAATTGTAAC 240
ACAATATTTA CTGCAAAAG AGCCACAGA GACATGTCAA TGAAGTCATA G 291
  
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human  
 (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Glu Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His
 1           5           10           15
Ser Gly Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg
          20           25           30
Val Glu Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp
          35           40           45
Ile Asp Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu
          50           55           60
Ile Val Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro
          65           70           75           80
Lys Gly Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala
          85           90           95
Leu Ile Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val
          100          105          110
Ser Ser Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn
          115          120          125
Leu Ser Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro
          130          135          140
Arg Lys Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val
          145          150          155          160
Glu Leu Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala
          165          170          175
Gly Ile Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg
          180          185          190
Val Ala Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg
          195          200          205
Phe Val Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile
          210          215          220
Leu His Phe Gly Lys Phe
225          230
  
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Gly Ser Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr
 1             5             10             15
Gly Ser Ile Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser
 20             25             30
Arg Arg Arg Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly
 35             40             45
Asp Arg Tyr Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg
 50             55             60
Glu Arg Arg Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly
 65             70             75             80
Asp Tyr Gly Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu
 85             90             95
Ser Lys Thr Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser
100            105            110
Asp Ile Arg Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp
115            120            125
Val Arg Leu Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser
130            135            140            143
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(B) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
Met Pro His Met Leu Ser Gln Leu Ile Ala Gly Gly Val Ser Thr Ser
 1             5             10             15
Cys Val Thr Ala Leu Gly Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr
 20             25             30
Leu Ser His Ala Ser Ser Pro Phe Ala Asp Leu Val Phe Cys Pro Phe
 35             40             45
Ala Glu Ile Asn His Ser Gln Glu Tyr Asp Asn Met Arg Gly Pro Val
 50             55             60
Ser Pro Pro Asn Lys Gln Phe Asn Leu Gly Val Ile Phe Gly Ile Pro
 65             70             75             80
Asn Asn Cys Arg Phe Pro Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu
 85             90             95
Leu Gly Asn Val Leu Asn Tyr Pro
100
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr
 1           5           10           15
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser
          20           25           30
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser
          35           40           45
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro
          50           55           60
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys
          65           70           75           80
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu
          85           90           95
Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys
          100          105          110
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe
          115          120          125
Thr Arg Thr Asp Ile
          130
  
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr
 1           5           10           15
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser
          20           25           30
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser
          35           40           45
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro
          50           55           60
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys
          65           70           75           80
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu
          85           90           95
Ser Leu Glu Pro Ala Phe Ala Glu His Trp Ser Gly Glu Phe Glu Lys
          100          105          110
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe
          115          120          125
Thr Arg Thr Asp Ile
          130
  
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly
 1             5             10             15
Glu Lys Leu Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg
          20          25          30
Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His
          35          40          45
Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp
          50          55          60
Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile
          65          70          75          80
Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile
          85          90          95
Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln
          100         105         110
Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro
          115         120         125
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
TCATGAAGTG AAGCCAACTG TTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT      60
ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGATCTGG ATTTTGTGCA TATGTGGAAT      120
CATAATTTAA ACAAATCAA CTAAGATGAT CCAAGTCCA CACAACTGCA CTTCAATATT      180
CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCACAAGAT TCTGAGCTGT CGTAAAAAGC      240
CTGGCTCGTG GTTCTATTT ATAGTGACA CATGTTGGGT TATAATCACA AACCTGGAAC      300
TCTGT                                           305
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAAACCACGG CTTACACCTA GAGACAGCAT TCAGATATAG ACGGGATACT TGTGTTAGTC	60
AGTTCCTTTA TAACAGGTGA ATCTCTCTCC CACTGCTTCA ACACTGCGTG ACAAAGCCAA	120
TTGGGAAGCA GCTTTACAAA TGTGACTTGA CTTGGGGATC TTCTTGATAC TTTGCCATGG	180
CAAGGAACAA GCCGCCTGAA CTAAATGCCA CTCCATTGA TTCCACGCTT AAAGTAACCA	240
TGCAACCGAC TATAGT	256

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TACTCTTCAA CCATGATTTT TCTCTGATGG CCTGTGTGAA CAGATTAATG GTGTCCATCT	60
AATTCCTTCC CCACTGGGGG AAAGCAAATC ATCAGGCCCA TTGCAAAAAC TGCTCTTGGT	120
TGAGCTTCCT GCCTTAAATC ATACCCACAG TGAATGGCGT CCCTTTATCA CCGCTAATGA	180
CTCTGACATC TCTCTCCACT CACATGTGAG CCTCCTCAGC TCTCGANAAA CAAGTCNGTC	240
TCGG	244

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCAGAAAA CTCCAGATCA AATGAGATGA GTATGGTGNN NAGGGCTGGC AATTAGAGGA	60
TACTCTCCAA TGGTGATGAA GGGAGATGTC TGGGGGAAAT CCAGCAGGAT GTTGATTTAG	120
TATGTACACA GTGAGAGGAT ACTTGTAGAG AACCTAGAAT CTTCTCTGAA TGTGACGGGC	180
CCTCAGAGAT AATTGTAAAC AGATAAGTGG ATGATTAAAT ACACTTCCTC CAGTAGGCTA	240
GATGTTAAGA CGGAGATC	258

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid; synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGCTTAATA TTATTCATAG ATCGAG	26
------------------------------	----

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
GTTATTATAC TATCAAGTAA CCCAAC 26

(2) INFORMATION FOR SEQ ID NO:45:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:  
GTGGATCTGG ATTTTGTCA TATGT 25

(2) INFORMATION FOR SEQ ID NO:46:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
GTTTGTGATT ATAACCCAAC ATGTG 25

(2) INFORMATION FOR SEQ ID NO:47:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
GAAGGGGAAG AGACATTAAA TTATC 25

(2) INFORMATION FOR SEQ ID NO:48:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
GCTTCTAAT CTCCTGAGTC ACTT 24

(2) INFORMATION FOR SEQ ID NO:49:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
GACAATGAGT AAGAAGAAAG AGGG 24

(2) INFORMATION FOR SEQ ID NO:50:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:  
 GTCCAGTCCC TTGGTTTATT TGTC 24

(2) INFORMATION FOR SEQ ID NO:51:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:  
 GGTACCCAGT TTCAAATTAA CATGG 25

(2) INFORMATION FOR SEQ ID NO:52:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:  
 GATTCTTCAA CTGCCAAACT TGTTT 25

(2) INFORMATION FOR SEQ ID NO:53:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:  
 GCTGATGCTT TTCTATCTGA CTTC 24

(2) INFORMATION FOR SEQ ID NO:54:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:  
 GACCAGGACT GAACAGAGGT GA 22

(2) INFORMATION FOR SEQ ID NO:55:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
GCTTATAGAC CATGTTTGTA GTAGG 25

(2) INFORMATION FOR SEQ ID NO:56:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
GTGAACAAAT GCTAAATCAG ACATG 25

(2) INFORMATION FOR SEQ ID NO:57:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:  
GCCACGGGTT TCCCATATCG AA 22

(2) INFORMATION FOR SEQ ID NO:58:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:  
GACTATACTT AGGAACCTCT GCAA 24

(2) INFORMATION FOR SEQ ID NO:59:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
GTTCTGCTCT CAGCAGATTG GTTA 24

(2) INFORMATION FOR SEQ ID NO:60:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
GCCAACATCT GAACTAAATA CTGC 24

(2) INFORMATION FOR SEQ ID NO:61:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:  
 GTTCAGTGAA TGTTACCTAG AAACA 25

(2) INFORMATION FOR SEQ ID NO:62:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  
 GGAGTGAAAA CTGTCTTGTT CATC 24

(2) INFORMATION FOR SEQ ID NO:63:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
 GTATGACAAA TAGTTTCTGC CTGAT 25

(2) INFORMATION FOR SEQ ID NO:64:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  
 GATTAACAAA GATGTACAGA CTGAG 25

(2) INFORMATION FOR SEQ ID NO:65:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:  
 GAGACAGCAT TCAGATATAG ACGG 24

(2) INFORMATION FOR SEQ ID NO:66:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
GCGTGGAATC AAATGGAGTG GC 22

(2) INFORMATION FOR SEQ ID NO:67:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:  
GATGGCCTGT GTGAACAGAT TAAT 24

(2) INFORMATION FOR SEQ ID NO:68:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:  
GAGAGAGATG TCAGAGTCAT TAGC 24

(2) INFORMATION FOR SEQ ID NO:69:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:  
GATCCCACACA ATTTCTTGTG ATTG 24

(2) INFORMATION FOR SEQ ID NO:70:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:  
GTTCCCCTAA AATAATGTGG TAATG 25

(2) INFORMATION FOR SEQ ID NO:71:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:  
GAGGATACTC TCCAATGGTG ATG 23

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:  
 GTCTTAACAT CTAGCCTACT GGAG 24

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:  
 GAGAGGAGCC ATGTATACAA ACCA 24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:  
 GCACGCAGGA TCAGATATAG TAATTC 26

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  
 GCTGAAACCT AAGCTGAAGG AAGG 24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  
 GTCCCTCACC TCAGATCACA CC 22

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:  
GCTATCTACC TGGCAGGAAA AGAG 24

(2) INFORMATION FOR SEQ ID NO:78:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
GAGTTTCTTA CTATGATCTG GATTC 25

(2) INFORMATION FOR SEQ ID NO:79:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:  
GCAAAATGTA CTCAGCTTCA ATCAC 25

(2) INFORMATION FOR SEQ ID NO:80:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
GTAAATGCAG TACTGTTCTG ATCC 24

(2) INFORMATION FOR SEQ ID NO:81:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:  
GAATGCTTCA TTCTCATTGT TTAAGG 26

(2) INFORMATION FOR SEQ ID NO:82:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:  
GTCAC TAGGA TTCCACAGAA CTTC 24

(2) INFORMATION FOR SEQ ID NO:83:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:  
 GAGGTAGGGC TTCCCTTCGC TA 22

(2) INFORMATION FOR SEQ ID NO:84:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:  
 GCATAACAAG TGACAGGGTT AGTTA 25

(2) INFORMATION FOR SEQ ID NO:85:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:  
 GGTGCTCCTT CCTTACTG GT 22

(2) INFORMATION FOR SEQ ID NO:86:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:  
 GACTACACAT AAACCCACCC CAG 23

(2) INFORMATION FOR SEQ ID NO:87:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
 GGGTACAGGA TTTCTAAGAA GTGG 24

(2) INFORMATION FOR SEQ ID NO:88:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
GGAGAAAATT TCAGTCATC TGAAG 25

(2) INFORMATION FOR SEQ ID NO:89:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:  
GCTGAAGTTA AGCATTATA CGCC 24

(2) INFORMATION FOR SEQ ID NO:90:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:  
GCGGCTGTAA TGTGCAATGA TGT 23

(2) INFORMATION FOR SEQ ID NO:91:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:  
GACAGCAACC TAATAACAGC TGTC 24

(2) INFORMATION FOR SEQ ID NO:92:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:  
GTCCTAGGCA CTTGTACTA GG 22

(2) INFORMATION FOR SEQ ID NO:93:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:  
GAGGGGACTT CCAAGAGTCT CT 22

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:  
 GTCTTCAGGA AAATTGTAGT TACAG 25

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:  
 GTTACAAACA CACACGAAGT TCCT 24

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
 GACTTCCTAA GGCACACTCA GC 22

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:  
 GTTAACTAC CTCTCAGGTC ATGA 24

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:  
 GTCGCCAAGG CTGTAGTGCA AT 22

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:  
GAAATAGGTA TCCCTTGATG TCGA 24

(2) INFORMATION FOR SEQ ID NO:100:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:  
GACCAAGAAT TCAGTTCATC AGTT 24

(2) INFORMATION FOR SEQ ID NO:101:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:  
GAATGAACCA GAGCCAGGAC AG 22

(2) INFORMATION FOR SEQ ID NO:102:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:  
GCCTTGATG TATGCCTGTG CC 22

(2) INFORMATION FOR SEQ ID NO:103:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:  
AAGAGTCCAC CAGGCATGG A 21

(2) INFORMATION FOR SEQ ID NO:104:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:  
TACCTTGTGT ACTTCTAGCT GAG 23

(2) INFORMATION FOR SEQ ID NO:105:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:  
GTTTTTTTTT TTTTTTA 17

(2) INFORMATION FOR SEQ ID NO:106:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:  
GTTTTTTTTT TTTTTTG 17

(2) INFORMATION FOR SEQ ID NO:107:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:  
GTTTTTTTTT TTTTTC 17

(2) INFORMATION FOR SEQ ID NO:108:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:  
CAGAGTGATG GATATCAA 18

(2) INFORMATION FOR SEQ ID NO:109:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:  
ATGAAAGTGC CAGTGTGCCA TG 22

(2) INFORMATION FOR SEQ ID NO:110:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:  
CCCATCACCA TCTTCCAGGA GC

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(2) INFORMATION FOR SEQ ID NO:111:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:  
TTCACCACCT TCTTGATGTC ATCATA

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